AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Please cancel the Sequence Listing as filed in the original application.

Please enter the substitute Sequence Listing set forth in Exhibit A on the next page (pg. 94) after the claims.

Please replace the paragraph beginning on page 31 at line 8 with the following amended paragraph:

To find the other AADH genes besides the genes obtained by the immunological screening as described above, the whole cosmid libraries of *G. oxydans* DSM No. 4025 in *E. coli* ED 8767 (*Sal*I-library and *Eco*RI-libraries) were screened by colony- and Southern-blot hybridization with a 0.9 kb *Sal*I fragment of p24D4. The 0.9 kb *Sal*I fragment hybridized with a oligonucleotide probe, ATGATGGT(GATC)AC(GATC)AA(TC)GT (SEQ ID NO: 13) synthesized according to an internal amino acid sequence of the natural AADH enzyme purified from *G. oxydans* DSM No. 4025, MetMetValThrAsnValAspValGlnMetSerThrGlu (SEQ ID NO: 14), which was obtained by digestion and sequenced by automatic gas-phase sequencer (Applied Biosystems 470A). The cells of the cosmid libraries were appropriately diluted and spread on LK agar plates, and the resulting colonies were blotted onto nylon filters and were analyzed by hybridization with the ^{32}P-labeled 0.9 kb *Sal*I fragment. About 1% of the colonies showed positive signals; 41 colonies were selected from the *Sal*I library and 20 from *Eco*RI library, and they were subjected to restriction enzyme analysis, followed by Southern-blot analysis. Six different AADH gene-related DNA regions were isolated in this screening as follows: four already-isolated regions carried on p24D4, p1E2, p26C3 and, p17E8, and two new regions carried on two separate plasmids designated as pSS31 and pSS53. The other plasmid pSS33 carried both of the two regions which were carried on p24D4 and pSS31.

Please replace the paragraph beginning on page 40 at line 20 with the following amended paragraph:

N-terminal amino acid sequences of the mature Enzymes A, A" and B were analyzed with automatic gas-phase sequencer (470A; Applied Biosystems) by Edman method [Acta Chem. Scand., 4, 283-293, {1959)]. The analysis of the Enzyme A' was not done because of an insufficient purity of the sample. The results were as follows:

Enzyme A : Gln-Val-Thr-Pro-Val-Thr---- (SEQ ID NO: 15)

Enzyme A" : Blocked N-terminal residue

Enzyme B : Gln- Val-Thr-Pro-Ile-Thr-Asp-Glu-Leu-Leu-Ala---- (SEQ ID NO: 16).

The determined sequences of Enzyme A and B were identical to the sequences (starting from the twenty-fourth residues) deduced from the nucleotide sequences described in SEQ ID NOS. 5 and 8; these results indicate that the initial 23 residues of the enzymes are the signal sequences. By analogy of the Enzymes A and B, the first 23 residues of Enzyme A' and A" are also deduced to be the signal sequences.